



**REPORT OF THE WORKSHOP ON DEEP-SEA TAXONOMIC  
STANDARDIZATION: STRATEGIC APPROACHES FOR COLLABORATION**

15-16 September 2020, Online

**INTRODUCTION**

1. In accordance with the UN Convention on the Law of the Sea (“the Convention”) and 1994 Agreement relating to the implementation of Part XI of the Convention, the International Seabed Authority (ISA), on behalf of the States Parties to the Convention, is mandated to administer the mineral resources in the Area and to control and organize current exploration activities, as well as future mining activities, in the Area for the benefit of mankind as a whole. The Authority is also mandated to take necessary measures with respect to activities in the Area to ensure effective protection for the marine environment from harmful effects and to adopt appropriate rules, regulations and procedures for, *inter alia*, the prevention, reduction and control of pollution and other hazards to the marine environment, the protection and conservation of the natural resources of the Area and the prevention of damage to the flora and fauna of the marine environment<sup>1</sup>.
2. In addition, the Authority is required to promote and encourage the conduct of marine scientific research in the Area, and coordinate and disseminate the results of such research and analysis when available<sup>2</sup>. The importance of this mission was highlighted by the Strategic Plan of the ISA for the period 2019-2023, adopted by the Assembly at its twenty-fourth session in 2018<sup>3</sup>. Especially through the strategic direction 4 (“*Promote and encourage marine scientific research in the Area*”), the members of the ISA have established the vision in this regard, which is being implemented according to the High-level Action Plan for 2019-2023 adopted by the Assembly at its twenty-fifth session in 2019<sup>4</sup>.
3. In 2017, the United Nations Decade of Ocean Science for Sustainable Development from 2021 to 2030 was proclaimed by the United Nations General Assembly in its resolution 72/73. In July 2020, the ISA developed an action plan<sup>5</sup> to formalize and organize its contribution to the implementation of the United Nations Decade, building on the strategic directions, high-level actions and associated outputs set out in the abovementioned Strategic Plan and the High-level Action Plan. The ISA Assembly has been invited to consider, with a view to adoption, this action plan at its subsequent session.
4. Among six strategic research priorities identified in the action plan, the following priorities highlight the importance of expanding deep-sea knowledge base and standardizing taxonomic information: 1) advancing scientific knowledge and understanding of deep-sea ecosystems, including biodiversity and ecosystems functions, in the Area; and 2) standardizing and innovating methodologies

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<sup>1</sup> United Nations Convention on the Law of the Sea, art.145

<sup>2</sup> United Nations Convention on the Law of the Sea, art.143

<sup>3</sup> [ISBA/24/A/10](#), annex, para. 29

<sup>4</sup> [ISBA/25/A/15](#)

<sup>5</sup> [ISBA/26/A/4](#)

for deep-sea biodiversity assessment, including taxonomic identification and description, in the Area.

5. In pursuance of the strategies and priorities identified above, the ISA, in collaboration with the Ministry of Oceans and Fisheries of the Republic of Korea (MOF) and the National Marine Institute of Korea (MABIK), convened an online workshop on Deep-sea Taxonomic Standardization: strategic approaches for collaboration, from 15-16 September 2020. The workshop was delivered via the Microsoft Teams platform.

6. The workshop aimed to identify coherent, collaborative, and scientifically robust solutions to addressing taxonomic knowledge gaps in various stages from collection, preservation, and archiving of biological samples and taxonomic data to identification and description of species. Specifically, the workshop focused on: (i) identifying specific needs and approaches to advance deep-sea taxonomic knowledge in various biotic groups (microbiota - to megafauna), including tools to be developed for targeting different types of uses and users; (ii) identifying existing institutions and initiatives that can provide taxonomic services, including molecular and morphological identifications, archiving facilities (online databases and curated natural history collections), and training on taxonomic skills, as well as their contributions to advancing deep-sea taxonomic knowledge; and (iii) exploring possible mechanisms for enhancing collaboration among contractors, academic/scientific institutions, and other stakeholders, including through developing or strengthening deep-sea taxonomic knowledge platforms, building on existing mechanisms, as well as facilitating sharing of data and expertise and long-term capacity development.

7. Drawing on the results of this workshop, the ISA secretariat can start developing a dedicated deep-sea taxonomic knowledge platform for the sustainable integration of taxonomic information, including through the ISA DeepData database. Likewise, the workshop provided an opportunity to establish partnerships to enhance sharing of data and expertise and promote research and capacity building on issues related to deep-sea taxonomy.

8. The workshop was attended by 127 participants in their individual expert capacities through online registration. The full list of workshop participants is provided in annex I to this report.

## **ITEM 1. OPENING OF THE WORKSHOP**

9. Mr. Michael Lodge, the Secretary General of the ISA, delivered his opening remark. He expressed his appreciation to the Ministry of Oceans and Fisheries of the Republic of Korea and the National Marine Biodiversity Institute of Korea for their support in the organization of the workshop. He also expressed his gratitude to the Executive Secretary of the Convention on Biological Diversity for her continued support towards the work of the ISA, and to the workshop co-chairs for their leadership in designing the workshop. Mr. Lodge highlighted the ISA's mandate on the protection of the marine environment from the potential harmful effects of exploration for and recovering of seabed minerals, as well as its duty to promote and encourage marine scientific research in the Area. He underlined the importance of data and information generated from deep-sea research in promoting the development of a robust regulatory framework supported by environmental standards and guidelines, while ensuring the quality of environmental impact assessments and regional environmental management plans. In this vein, he stressed the need to strengthen the collective scientific knowledge of deep-sea biodiversity, which has been recognized by the ISA's Strategic Plan and the High-Level Action Plan for 2019-2023. He then introduced the ISA Action Plan in support of the UN Decade of Ocean Science for Sustainable Development to be considered by the Assembly in October 2020, which identified standardization of methodologies for deep-sea biodiversity assessment, including taxonomic identification and description in the Area, as one of the six strategic research priorities. Lastly, he emphasized the importance of this workshop as its outputs would directly contribute to the work of the ISA secretariat in initiating concrete efforts towards establishing a global platform for collaboration in

facilitating effective generation, use, and sharing of deep-sea taxonomic information.

10. Mr. Woon-yul Oh, Deputy Minister of the Ministry of Ocean and Fisheries of the Republic of Korea delivered his opening statement. He began by thanking the Secretary General of the ISA and the president of the National Marine Biodiversity Institute of Korea for co-hosting the workshop. He extended his gratitude to the Executive Secretary of the Convention on Biological Diversity for her support in this workshop, and to the workshop co-chairs for their contributions. While acknowledging various challenges in accessing deep-sea, Mr. Oh stressed the need to expand collaborative efforts in deep-sea research. In this regard, he highlighted the relevance of this workshop and the importance of its role in facilitating discussions to strengthen cooperation and capacity-building for deep-sea taxonomy research at the global level. He concluded by stating that the Government of the Republic of Korea will actively promote efforts towards the advancement of research in the field of deep-sea taxonomy.

11. Mr. Sun-do Hwang, the President of the National Marine Biodiversity Institute of Korea (MABIK) delivered his opening remarks. He first expressed his gratitude to the Secretary General of the ISA for co-organizing the workshop, the Ministry of Oceans and Fisheries of the Republic of Korea for sponsoring it, and the Executive Secretary of the Convention on Biological Diversity for promoting collaboration to advance deep-sea taxonomy. He also thanked the workshop co-chairs for their support. Mr. Hwang emphasized that taxonomic knowledge forms the basis to understanding biological interactions between species and ecosystems. He highlighted that MABIK has been contributing to developing marine taxonomy by collecting, preserving, and studying marine species and specimens. He also underlined the need for an effective mechanism to collaborate and build capacities for the advancement of deep-sea taxonomy, especially given the unique challenges associated with deep-sea research despite its importance. In this regard, he brought the participants' attention to MABIK's forthcoming training program called "Global Women's Leadership Training Program in Marine Bio-Resources Information System", which aims to foster female researchers' capacity in marine taxonomy and other closely related fields. Lastly, he stated that MABIK would continue to promote deep-sea taxonomy in close collaboration with the ISA secretariat and invited the participants to use the workshop as an opportunity to enhance collaboration for improving the knowledge base of deep-sea biodiversity.

12. Ms. Elizabeth Maruma Mrema, the Executive Secretary of the Convention on Biological Diversity, delivered her opening statement. She began by expressing her appreciation to the ISA for organizing the workshop. Recognizing the importance of alignment and coordination among various frameworks for the ocean in achieving their respective goals, she stated that the CBD has been prioritizing mainstreaming of biodiversity across different sectors and international processes. In this regard, she noted previous collaborative efforts between the CBD secretariat and the ISA secretariat towards CBD's work on ecologically or biologically significant marine areas, biodiversity-inclusive environmental impact assessment, and the Sustainable Ocean Initiative. She then highlighted that the collaboration can be expanded through the CBD's Global Taxonomy Initiative. Ms. Mrema acknowledged that both the ISA and the CBD are at a critical time when the foundation for the future work is being established. She elaborated that ISA's current work on deep-sea taxonomy, mining regulations, and regional environmental management plans, will lead to the creation of a global framework for sustainable deep-sea mining in the Area, while the ongoing development of the post-2020 global biodiversity framework under the CBD will set goals and targets for a sustainable future for biodiversity. Lastly, she emphasized that participants' contributions in this workshop on strengthening networks of deep-sea taxonomists will enhance the necessary alignment and coordination for the global community to move together towards the common goals of biodiversity conservation and sustainable use.

## **ITEM 2. WORKSHOP BACKGROUND, SCOPE AND EXPECTED OUTPUTS**

13. The workshop was organized in plenary and breakout-group sessions. The workshop co-chairs Gordon Paterson (member of Legal and Technical Commission of the ISA) and Peter Ng (Lee Kong Chian Natural History Museum, Singapore) moderated the workshop deliberation.
14. Under this item, participants had before them following documents prepared by the ISA secretariat: (i) draft Action Plan of the International Seabed Authority in support of the United Nations Decade of Ocean Science for Sustainable Development; and (ii) draft background document to compile scientific information relating to the workshop objectives.
15. Jihyun Lee and Luciana Genio (ISA secretariat) provided a presentation on workshop background, scope and expected outputs.
16. Summary of the above presentation is provided in annex II to this report.

## **ITEM 3. SETTING A CONTEXT FOR DEEP-SEA TAXONOMIC STANDARDIZATION**

17. Under this item, Gordon Paterson delivered a presentation on “Deep-sea taxonomy within the context of the ISA: challenges and opportunities”.
18. Participants exchanged their views, insights and suggestions in response to the presentation. Some participants addressed the need to secure financial sustainability for continued upgrade of cyberinfrastructure and additional personnel to manage growing digital resources. The importance of taxonomy for society and its relevance for biodiversity studies were also highlighted.
19. Summary of the above presentation is provided in annex II to this report.

## **ITEM 4. OVERVIEW OF NEEDS AND APPROACHES FOR ADVANCING DEEP-SEA TAXONOMIC KNOWLEDGE WITHIN THE CONTEXT OF ISA**

20. Under this item, the following presentations were delivered on two different themes, with a view to identifying needs and appropriate approaches for advancing deep-sea taxonomic knowledge within the context of the ISA:
  - Theme 1: Building references databases, collections, and libraries: sharing and archiving of taxonomic information:
    - Tammy Horton (World Register of Marine Species-WoRMS)
    - Pedro Martinez Arbizu (Senckenberg Research Institute, Germany)
  - Theme 2: Developing tools for biodiversity assessment and monitoring: automated image analysis and environmental DNA (eDNA)
    - Kerry Howell (Plymouth University, UK)
    - Masaki Miya (Natural history Museum and Institute, Japan)
21. Summaries of the above presentations are provided in annex II to this report.
22. Participants exchanged their views, insights and suggestions in response to the above-noted presentations. Some participants highlighted the followings, *inter alia*:

- **Formal (Linnean) and non-formal (interim names for ‘dark taxa’) nomenclature.** The need for developing and adopting a consistent coding system (Open Nomenclature) was highlighted. It is also important to distinguish clearly the “temporary names” that are given to undescribed species, from those that are given during identification processes. The two types of names must have different and recognizable forms: names for taxa that are known to be new to science (lack of general knowledge), and names for taxa of which identity is unknown (lack of particular knowledge).
- **The use of an online platform for sharing “temporary names” associated with brief descriptions and linked to authors** was suggested to ensure effective communication, while preserving authority. For instance, the global database WoRMS already allows the inclusion of species with interim names in special cases. The possibility to include all available non-formally named species until they become formally described is currently being considered by the WoRMS Steering Committee. This would help to identify rare species, as they may remain non-formally named indefinitely. This would also represent an increased demand for new taxonomic editors, which are responsible to enter and validate species names and taxonomic information in the database (currently on a voluntary basis).
- **Vouchering specimens at natural history collection repositories** is key for biodiversity studies, particularly the specimens used on Environmental Impact Assessments (EIA). The way to archive and preserve specimens for long-term needs to be considered when estimating costs. It is also necessary to support small biological collections, which are lacking financial and expertise resources. It would however be more economically efficient to provide support in an organized network framework at national or regional levels.
- **Creation of reference DNA libraries** in areas of future exploitation activities could be facilitated by the ISA, contractors, and academia.
- **Storing imagery data** is very challenging due to digital space constraints. The experience of large scientific programmes that commonly manage great volumes (petabytes) of data such as those in space, atomic or meteorology domains needs to be considered as an example for the deep sea.
- **A common protocol to archive videos and photographs** needs to be developed alongside species annotations. These data need to be systematically published to allow revisions by taxonomists.
- **Accuracy of Artificial Intelligence (AI).** Annotating images is directly linked to the data it is trained on. If the data have been interpreted by a taxonomist, the training data quality will be better, and thus AI may perform better.
- **Mechanisms for intercalibration among different databases** need to be established.
- **Opportunities for capacity development** in computer sciences and other data scientists need to be promoted to contribute and increase collaborations in expanding image and video repositories and collections, as well as in developing software and technologies. Future video-based studies need to involve collaboration between taxonomists and ecologists.

23. Participants were then split into four groups to undertake focused discussions in breakout sessions, each focusing on a major faunal group, and building on the ideas, examples, and experiences provided by the theme presentations.

- Microbiota / eDNA
  - Facilitated by: Xue-Wei Xu (Second Institute of Oceanography of the Ministry of Natural Resources, China)
  - Rapporteur: Jason Smith (Nauru Ocean Resources Inc (NORI) / Deep Green Metals)
- Meiofauna

- Facilitated by: Daniela Zeppilli (French Research Institute for Exploration of the Sea -IFREMER, France)
  - Rapporteur : Ann Vanreusel (Ghent University)
  - Macrofauna
    - Facilitated by: Adrian Glover (Natural History Museum of London, UK)
    - Rapporteur: Muriel Rabone (Natural History Museum of London, UK)
  - Megafauna
    - Facilitated by: Erik Simon Lledo (National Oceanography Centre, UK)
    - Rapporteur: Merlin Best (Department of Fisheries and Oceans, Canada)
24. The following set of questions were considered during the breakout sessions:
- Theme I
    - How can quality assurance/control of taxonomic data be ensured? For example, the role of voucher specimens, samples, and data curators, and intercalibration exercises.
    - What are some actions/steps (short-term and long-term) needed to advance taxonomic knowledge in a standardized manner?
  - Theme II
    - Which tools are required to improve species identification in different mineral provinces currently under exploration?
    - What initiatives, networks, and resources are available, desirable, and/or needed to support key taxonomic groups?
25. Results of the group discussions during the breakout session are summarized in annex III to this report.
26. Each group delivered a brief presentation at the plenary on the outcome of their respective breakout group discussion, including ways and means to promote effective integration of deep-sea taxonomic information into efforts towards sustainable development within the context of the ISA.
27. Participants at the plenary exchanged their views, insights and suggestions in response to the results of the break-out session group discussion. Some participants highlighted the followings, *inter alia*:
- ***Availability of historical literature and images in an open access format*** (e.g., digitalization of very old books). Current initiatives, such as Biodiversity Heritage Library and WoRMS, need to be reinforced.
  - ***Revisiting type material deposited in natural history museums in a historical perspective.*** Integration of historical material (notably type specimens of early described deep-water species) into modern taxonomic tools (e.g., molecular data) is very difficult but critical. There are few local examples which could be used as a model in a global scale context.
  - ***Wider distribution of biological collections for broader access to physical specimens and capacity development.*** Use of developed tools in informatics (e.g., standardized data formats such as DarwinCore, barcoding, etc.) can facilitate small institutions to hold sampled material and make the data accessible.
  - ***Capacity building and training program in taxonomy*** need collaboration of all actors involved in deep-sea mineral resource activities.

**ITEM 5. EXPLORE POSSIBLE MECHANISMS FOR COLLABORATION TO SUPPORT DEVELOPMENT OF A DEEP-SEA TAXONOMIC KNOWLEDGE PLATFORM, AND NECESSARY LONG-TERM CAPACITY DEVELOPMENT WITHIN THE CONTEXT OF ISA**

28. Under this agenda item, the following experts from various backgrounds and expertise shared in a panel discussion their ideas and insights on ways and means to enhance collaboration and contribution to the development of a deep-sea taxonomic knowledge platform:

- Tim O’Hara (Natural History Museum Victoria, Australia)
- Chong Chen (Japan Agency for Marine-Earth Science and Technology-JAMSTEC, Japan)
- Samantha Smith (Global Sea Mineral Resources-GSR, Belgium)
- Koh-Siang Tan (Ocean Mineral Singapore-OMS, Singapore)
- Tina Molodtsova (P. P. Shirshov Institute of Marine Biology of Russian Academy of Sciences, Russia)
- Magdalena Błażewicz, (University of Lodz, Poland)
- Sarah Samadi (Museum of Natural History, France)
- Mauricio Shimabukuru (ISA Secretary-General Awardee, Brazil)
- Jinwook Back (National Marine Biodiversity Institute of Korea-MABIK, Republic of Korea)
- Ward Appeltans (Ocean Biodiversity Information System-OBIS)

29. Summaries of the above panel presentations are provided in annex IV to this report.

30. Participants exchanged their views, insights and suggestions in response to panel discussion. Some participants highlighted the followings, *inter alia*:

- Need to increase awareness among potential donors and funding agencies, as well as among industry sectors, of taxonomy as essential science supporting other scientific fields related to biodiversity. It was clarified that the ISA has provided recommendations for properly archiving biological samples and storage institutions, such as public and private natural history museums, to be actively involved. These institutions, however, may not be interested in curating this kind of collection without financial support, because long term maintenance of biological samples is expensive, both in human as well as other resources (e.g., preservatives, consumables, databasing and space). Financial requirements relating to curation and maintenance of repositories in natural history museums or other long-term storage facilities need to be considered within the context of activities in the Area.
- Archiving specimens in scientific collections around the world, with at least high taxonomic level identifications, including also small institutions, which could curate deep-sea specimens and allow loans to taxonomists. Setting an annual contractor target for museum vouchering (including costing it) was suggested.
- Taxonomic work is a two-stage process and there is a need to provide training for personnel sorting the specimens and identifying species based on taxonomic tools (‘identifiers’ or parataxonomists), and those who describe species (taxonomists). The creation of platforms for identifications before sending specimens to taxonomists for verification was suggested.
- Intercalibration exercises are fundamental requirement to assess biodiversity and undertake environmental baseline studies. Maintenance of high-quality identifications, while keeping

names of taxonomists and identifiers associated to identified species, would reduce variations in accuracy among identifiers.

- Reduced number of taxonomists worldwide is due to insufficient job opportunities. Trained young taxonomists often move to other fields (e.g., ecology), because of the lack of jobs in the field of taxonomy. Moreover, natural history museums have an increasing tendency to choose scientists with genetic/DNA expertise and/or high-impact research domains (e.g., data analytics and climate change science) over organismal taxonomists.
- Limited number of well-trained curators. Most biological collection personnel are trained on the job. Relevant scientific training (e.g., specimen collection, verification, preparation, curation, and maintenance) takes place in biology and natural history courses on specific organismal groups, although these types of courses are also in decline. A small number of museum studies programmes offer formal degree or certificate programmes for natural history collection work.
- Promotion of regional capacity building and regional workshops was suggested, taking into account the need for specialists on each phylum at the regional scale.
- One possible way to financially support taxonomy is by making it as part of regulatory requirements (e.g., EIA or EMMP).

## **ITEM 6. SUMMARY AND CONCLUSION**

31. The workshop co-chairs provided a summary of the workshop results, including suggested approaches to promote effective integration of deep-sea taxonomic information into efforts towards sustainable development within the context of the ISA. The following was highlighted:

- There was a clear emphasis that a range of competent expertise is necessary. Training activities should be diversified, including training programmes combining experienced and early career taxonomists, as well as training activities for parataxonomists (i.e., sorters and identifiers) and users of taxonomy (i.e., ecologists, other scientists, etc.).
- Access to specimens and samples is essential. A de-centralized physical infrastructure for safeguarding physical collections (small scientific collections and national natural history museums) could be less risky and more economically efficient. The cost for using such repositories needs to be considered early to be sustainable in the long term.
- A global digital platform interlinking multiple databases is crucial. The ISA DeepData can play a central role as a primary source of data from and for ISA contractors.
- The efforts for resource mobilization should include engaging not only the contractors but also the sponsoring States, and all members of the ISA. Creating synergies and collaboration among existing programmes at the ISA, and other global initiatives (e.g., OBIS-IOC/UNESCO, WoRMS) as well as other UN/international organizations (e.g., CBD, FAO, IMO, RFMOs etc.) would accelerate consolidated efforts for addressing taxonomic issues.
- Raising awareness of the importance of taxonomy with various stakeholders including civil society groups is fundamental for enhancing knowledge of deep-sea biodiversity and sustainable development of activities in the Area.

## **ITEM 7. CLOSURE OF THE WORKSHOP**

32. The workshop was closed at 10:00 a.m. on Wednesday, 16 September 2020.

*Annex I*

**List of Participants**

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*Annex II*

**Summary of Theme Presentations**

***Presentations delivered under agenda item 2***

**Workshop background**

**By Jihyun Lee (ISA Secretariat)**

The protection of the marine environment from harmful effects which may arise from activities in the Area is at the core of ISA's mandates. In terms of link between science and policy, ISA's environmental management also represents a notable example of global marine governance. Almost 40 years of continuous scientific activities undertaken by pioneer investors and contractors during the exploration of deep sea minerals, both before and after the entry into force of the UN Convention of the Law of the Sea represent a major contribution to collective knowledge of deep sea environment including taxonomic knowledge. Under the exploration contract, contractors are obliged to gather information on environmental baseline. These data will serve as the primary inputs into the environmental impact assessment (EIA) process as part of the future application for exploitation contract.

The ISA global data repository, called DeepData, contains data and information related to mineral resources, as well as biological, physical, and geochemical parameters of the marine ecosystem, from the seafloor to the ocean surface. Environmental data including taxonomic data and information provide the critical scientific basis for the ISA in fulfilling its mandate for the protection of the marine environment in the Area. In addition to EIA, as well as environmental monitoring and management system to be undertaken by the contractors within their contract area, the ISA has developed environmental plans at regional scale since 2012. Regional Environmental Plans provide a proactive framework for identifying environmental management and tools at regional scale including area-based management tools, and scientific approaches to address cumulative impacts and adaptive management.

In support of the UN Decade of Ocean Science for Sustainable Development, the ISA secretariat has prepared an action plan for Marine Scientific Research which will be considered by the Assembly in the forthcoming session. This action plan identifies six scientific research priorities (SRP) as aligned with the ISA Strategic Plan and High-level Action Plan for the period of 2019-2023. While all SRPs are relevant for the theme of this workshop deliberation, the second SRP highlights ISA's focus to facilitate collaborative efforts among different contractors, scientific institutions, natural history museums and other stakeholders to standardize and innovate methodologies for deep-sea biodiversity assessment. It is very critical to establish a coherent set of scientific reference for species identification, description, and classification in support of collective efforts for biodiversity conservation and environmental protection in the Area.

**Workshop scope and expected outputs**

**By Luciana Genio (ISA Secretariat)**

The ISA has undertaken several activities addressing issues related to taxonomic standardization, which have primarily focused on the biological communities found in the Clarion Clipperton Zone. Building on the outcomes of those activities, this workshop will extend the discussions to all geographic regions where exploration of mineral resources is currently taking place by contractors, including all three types of mineral resources (polymetallic nodules, sulphides and cobalt-rich crusts) and their associated habitats. Further consideration should also be given to less known communities found in midwater environments.

The focus of the workshop is relevant to all taxonomic groups and addresses shared and/or specific concerns related to different methodological approaches used to sample and identify various organisms, which are commonly adapted to their size classes (i.e., microbiota, meiofauna, macrofauna and megafauna). In the context of the workshop background, previously presented by the secretariat, the workshop aims to identify existing and future needed approaches and tools, as well as physical and digital infrastructure to improve standardization of taxonomic data and information in a scientifically robust, coherent, and collaborative way. It is expected that key elements needed to start developing a dedicated deep-sea taxonomic knowledge platform for sustainable integration and coordination of taxonomic data and information will be identified. These elements may include enhancing the existing or establishing new expert networks and partnerships, for example for data curation and development of identification toolkits to support taxonomic identifications and descriptions. They may also include finding solutions to establish links among existing databases and other platforms to coordinate the increasing amount of taxonomic information (e.g., from molecular and image-based approaches), making the data accessible to all. Another important aspect to be considered is future activities for capacity development in deep-sea taxonomy.

***Presentations delivered under agenda item 3***

**Deep-sea taxonomy within the context of the ISA: challenges and opportunities**

**By Gordon Paterson (member of the Legal and Technical Commission)**

Within a regulatory framework, standardization is paramount. Standardization ensures consistency of data resulting from the research activities of various scientific and commercial groups, allows the data to be validated and corroborated by wider audiences, and enables authentication when regulations and recommendations are issued. The ISA has provided recommendations on the collection of environmental baseline information, which are usually implemented by contractors. These recommendations were developed by the Legal and Technical Commission with inputs from many experts, gathered during different taxonomic workshops. Contractors submit data to the ISA through their annual reports. The ISA needs to assess the information being generated, including consistency of the data across time and space to support various regulatory and management decisions. One of the key activities that require standardized taxonomy is the development of regional environmental management plans. Likewise, contractors need to develop good taxonomic data during environmental baseline studies, which will form the basis for Environmental Impact Assessment (EIA). Access to taxonomic expertise is critical and often challenging for the contractors over the time frame of their exploration contract, that can last 15 years or more in nodule areas. The best available evidence in the taxonomic context is the publication of taxonomic results including new species (gold standard). The second most important piece of evidence is the sampled specimen itself or a derivation of it (e.g., DNA extract and sequence); specimens are the only proof available to check the data and subsequent ecological analysis (auditable verification). So, the curation and preservation of specimens need to be properly resourced. New technologies and techniques can be used to enhance taxonomic information. For example, the rapid development of computer sciences and molecular biology have rejuvenated taxonomy research. While the ISA can only recommend approaches that are widely accepted by the scientific community and have demonstrated to be consistent and standardized between users, it needs to be aware and cognisant of the new technologies. To ensure high quality taxonomic outputs, standards must be set and enforced. As the activities evolve to routine monitoring, the productive partnerships between contractors and academia may not last. Maintaining and sustaining taxonomy in the future is vital, and all stakeholders within the ISA (ISA members, contractors, scientific community) need to be involved to support long-term cooperation, access to infrastructures, taxonomic services and expertise, as well as training.

***Presentations delivered under agenda item 4***

**Theme 1: Building references databases, collections, and libraries: sharing and archiving of taxonomic information**

**The World Register of Marine Species (WoRMS): The importance of stable nomenclature in a world of dark taxa.**

**By Tammy Horton (World Register of Marine Species)**

Species-level identifications and a robust, clear taxonomic nomenclature are needed to allow comparisons across datasets, surveys and monitoring of impacts. Taxonomic nomenclature, the names given to species, allow referring to the fauna being studied in a consistent manner. In using a robust taxonomic nomenclature, it is possible to understand which species is being referred to, and discuss what species are found when and where. The World Register of Marine Species (WoRMS: [www.marinespecies.org](http://www.marinespecies.org)) brings these names together in one place, providing “An authoritative classification and catalogue of marine names” openly accessible to all. The use of WoRMS names helps to ensure taxonomic consistency by providing the most up-to-date name of the species encountered in faunal surveys. WoRMS nomenclature is also used by other systems, linking OBIS & GBIF & Genbank & BOLD using the unique APHIA ID applied to every name in the database. Editors are the driving force of WoRMS; there are currently over 500 editors in total, of which almost 300 are taxonomists. These taxonomic experts are supported by the Data Management Team at VLIZ in Belgium and this collaboration is behind the success of WoRMS.

Despite the availability of a robust nomenclatural database of known marine species, the numerous new (unnamed) taxa encountered in the deep sea still pose a problem – how to deal with these ‘Dark Taxa’? There is a growing number of taxa without formal scientific names and less than half of newly sequenced invertebrate taxa added to GenBank are identified to species level (i.e. have names) (Page, 2016). Scientific names are the foundation of science, a means to communicate about biodiversity. The need to document this diversity is proliferating in these ‘dark taxa’. Open Nomenclature can provide a means to communicate about unknown taxa, but it also needs to be managed in a standardized way. A standardized set of terms is already in use in taxonomic works (cf., aff., indet., inc., stet., see Sigovini et al., 2016), but it is necessary to ensure these are applied correctly and consistently to communicate about ‘dark taxa’.

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**By Pedro Martinez Arbizu (Senckenberg Research Institute, Germany)**

Species are the actors at the community level. Future deep-sea mineral exploitation will directly affect this component of the deep-sea habitats. At the population level, genes are the actors being interchanged among individuals of the same species. Species counts provide the basic information for the calculation of ecological variables, such diversity, turnover, connectivity or recovery, which are needed to assess possible impacts by exploitation of mineral resources and the recovery potential of deep-sea communities. In the abyss, most of sampled species are new to science (< 90 % in some groups) and are not formally described. The scientific names are the universal code used to exchange species-level information since Linnaeus. Currently, a genetic code or genetic barcode has been widely used to identify and refer to species and to exchange information about them. The workflow for preparing reference libraries includes the specimen, which can be identified and classified based on morphology, photographic documentation from field and laboratory observations, the associated sample metadata (e.g., location and date of sampling, etc.), and a piece of specimen tissue for extracting and sequencing DNA. In this workflow, six types of information

have been identified, which require different types of storage or collection, including: i) natural history collections, for storing voucher (type material) specimens; ii) image databases, for *in situ* and laboratory image of vouchers that are essential for quality control of genetic information (e.g., Biigle or BOLD); iii) databases for location/distribution information and associated metadata (e.g., OBIS); iv) tissue banks; v) DNA banks; and vi) databases for the DNA sequences (e.g., GenBank or BOLD). Recently, some large natural history museums offer the possibility to store frozen tissue and genetic material (-20°C or -80°C), but this still poses logistical constraints. More often, the tissue and extracted DNA remain with the researcher or the institution and are not made publicly available. Sequences databases are repositories where genetic sequences are stored, and also provide features for querying and matching sequence data. For instance, BOLD also stores voucher information, images, and other metadata associated with genetic information. In contrast to single sequences, New Generation Sequencing (NGS) generates millions of sequences that are stored in specialized databases, but currently it is not easy to compare data between different NGS projects. Currently, the genetic reference databases are very incomplete allowing only limited number of sequences to match at the species level. It is necessary to invest in genetic barcoding of deep-sea species representatives, associated to morphological identifications of high quality, to populate genetic reference libraries, such as BOLD and GenBank databases.

## **Theme 2: Developing tools for biodiversity assessment and monitoring: automated image analysis and environmental DNA (eDNA)**

**By Kerry Howell (Plymouth University, UK)**

The use of cameras, imagery and video as a means to survey and monitor the marine environment has seen rapid growth over the last 20 years. It began with the use of drop-down and towed camera systems and has now progressed to use of Remotely Operated Vehicles and Autonomous Underwater Vehicles. These new technologies can produce vast datasets of imagery and video of seafloor communities, providing the ability to gather rapidly new raw data on the deep-sea ecosystem. However, interpretation of this imagery is challenging. Image and video analysis is very time consuming and represents a major bottleneck in the interpretation of newly acquired data. There are no formal keys, training materials or standards on the identification of benthic taxa *in situ*. As a result, individuals, labs, and projects tend to create their own image reference libraries by which identification is standardized. In addition, analysis is a repetitive task in which observers become quickly tired, bored, and prone to making errors. Individuals will have an observer bias and that bias will be different between observers. The end-result is that it is often impossible to combine datasets between observers, limiting the onward use of data for management purposes at regional scale.

Artificial intelligence (AI) and computer vision (CV) offer a possible means to speed up data analysis and minimise observer bias. There are now many open source tools available and they are becoming easier to use, although still require some knowledge of programming. Initial tests of this technology based on an AUV dataset from the North Atlantic have shown promising results. Piechaud et al., (2019) used an open source AI, trained on sets of images annotated by a human, and then tested on new images to investigate AI performance. These authors were specifically interested in the following: the number of images required in order to train an AI to a given level of performance; and how performance of the AI changed depending on taxon richness (number of classes to choose from). The results suggested that the more training images provided, the better the AI performed, but performance plateaued, after which further human annotation for training purposes was wasted effort. This plateau occurred somewhat short of 100% performance. In addition, the AI performed better when it had fewer taxa to choose between, performance was excellent for some taxa but for others it was never good.

These findings suggest that open source AI may provide a useful tool to support the analysis of imagery and video in future, but there are challenges. The main challenge lies in the lack of a standard image reference library for use in the annotation of images and video, resulting in the inability to integrate human

annotated datasets into larger AI training datasets. To overcome this issue, a framework for the development of a global standardized marine taxon reference image database (SMarTaR-ID) to support image-based analyses has been proposed (Howell et al., 2019), and a web-accessible database is currently under development as part of the One Ocean Hub project. The database will be launched in January 2021 to coincide with the start of the Ocean Decade. However, further challenges remain, including the need to improve both the coverage and quality of training data, and thus imagery within the SMarTaR-ID database. A coordinated effort is required by the deep-sea community (academics, industry, NGOs) to photograph animals *in situ*, sample the animal, and have the animal identified and barcoded by a professional taxonomist, in order to improve understanding of how different taxa appear *in situ*, and provide the raw information for the development of field keys rather than just image libraries. Observers need formal training on field identification of animals in order to improve the quality of training data available. Robust quality control procedures need to be designed and implemented, including regular inter-calibration exercises, and repeated analysis of subsets of data, in order to ensure training data quality. Finally, there remains a need for the development of better AI and CV algorithms to improve overall performance.

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**MiFish eDNA metabarcoding: A new biodiversity monitoring method enables simultaneous detection of multiple fish species from a bottle of seawater**

**By Masaki Miya (Natural History Museum and Institute, Chiba, Japan)**

Environmental DNA (eDNA) is the extra-organismal genetic materials suspended in environmental samples, such as water and sediment. eDNA is shed from macro-organisms through faeces, body mucus, blood, and sloughed tissue or scales and has emerged as an alternative data source for biodiversity monitoring. By filtering a certain amount of water, eDNA is concentrated and captured on the filter membrane, from which it is extracted and subjected to various molecular biology experiments for detection of organisms. In particular, the eDNA metabarcoding approach enables simultaneous detection of multiple species using a high-throughput next-generation sequencing (NGS) platform. This approach co-amplifies a short fragment of eDNA from the target taxa (e.g., fishes) using a set of universal primers through PCR and then appends various adapters and index sequences to both ends of the amplified fragments (amplicons). Various combinations of different index sequences enable massively parallel sequencing using the NGS platform, with an output comprising tens of millions to billions of amplicons from multiple sampling sites. After data pre-processing and subsequent taxonomic assignment using a bioinformatics pipeline, a tentative taxonomic list becomes available for each sampling site. Our research group has attempted this biodiversity monitoring approach to deep-sea fishes using MiFish primers designed on the mitochondrial 12S rRNA gene (Miya et al. 2015). Seawater samples were taken from a deep-water pumping facility at Kumejima Island, southern Japan, where deep water was continuously pumped up from 612 m depth. Preliminary results showed that MiFish eDNA metabarcoding successfully detected >150 deep-sea fishes with varying size from 30 mm to >3 m in total lengths. If a large amount of seawater can be filtered (e.g., 50 L), MiFish eDNA metabarcoding can be a very effective approach for biodiversity monitoring of deep-sea fish.

*Annex III*

**Results of workshop discussions on needs and approaches for advancing deep-sea taxonomic knowledge within the context of the ISA**

***Microbiota / eDNA***

1. Definitions of microbiota and eDNA were provided as per the ISA guidelines. Microbiota are organisms invisible to the naked eye, smaller than meiofauna; operationally defined as organisms <32 microns in size. eDNA is one recognized tool for biodiversity monitoring through the use of metagenomic or amplicon sequencing approaches (e.g., of bacteria, archaea, viruses, fungi, protists, meiofauna). Participants were reminded that sampling and discussions should include midwater and the seabed ecosystem.

**Theme I: Q1. How can quality assurance/control of taxonomic data be ensured, including through the role of voucher specimens, sample and data curators, and intercalibration exercises?**

2. Participants noted that a library for isolated species is needed for microbiota taxonomy. It was highlighted that the standard approach for sampling bacterial communities is a PCR-based amplification of marker genes, usually using the 16S rRNA gene. It was suggested that the whole genome could be used essentially for taxonomy, due to a stronger taxonomic structure rather than a single marker gene. The 16S rRNA gene is not a single copy, and it has the advantage of a large database for 16S rRNA gene being available. Another suggestion was to find a balance between what can be matched with 16S rRNA gene and what can be obtained with genomes.

3. A question was raised about using genomes to delineate taxonomic groups. Using Hi-C libraries would be useful. It allows the study of DNA within the cell and the understanding of gene sequences in vicinity of the targeted gene. Participants agreed that this could be a useful approach to studying uniqueness of individual cells without having to separate out the cells from one another. However, it would require a separate library that will not be cross-linked with other libraries. Adding the environmental data (e.g., salinity, depth, etc.) to such samples would help to resolve ecotypes.

**Theme 1: Q2. What are some actions / steps (short-term and long-term) needed to advance taxonomic knowledge in a standardized manner?**

4. The importance of scale was noted by participants, as the sampling for obtaining eDNA would be different for seawater and sediment. Participants suggested that different sampling scales should be used. A question was then posed about how to develop a standardized method to enable widescale surveys of communities in these unknown systems. Participants discussed if 16S amplicon sequencing or another method should be used.

5. In water samples, there is often not enough DNA quantity, so it must be concentrated. In sediments, there are co-eluted inhibitory factors. Contracting out should include assessment of who is suitable to carry out the work, as the samples can be neglected, or the amplification inhibited. It is hard to determine the level of inhibition, even with advanced techniques like mass spectrometry. The 260/280 ratio is often used, but it does not always provide a clear picture of potential inhibition either.

6. A question was also raised on how to remove hydrocarbons found in samples as some researchers face challenges with this type of inhibitors. Dilution was identified as the primary way to solve this problem, perhaps using proper phenol-chloroform extraction.

7. Target gene for V3-V4 Illumina for 16S rRNA gene would be a good high throughput approach. It was highlighted that there are not many tools except for these approach for analyzing microbial communities right now.

8. It was mentioned that contractors are required to submit environmental data collected to the ISA, which are then hosted by the ISA database DeepData. Specialized databases were also considered important in taxonomy. Ongoing collaboration and discussion about dataflow between DeepData and other databases, such as OBIS/IOC-UNESCO were noted. Participants discussed whether a dataflow between DeepData and other public taxonomic databases such as GeneBank could be implemented. This discussion can be pursued within the ISA.

9. A question was raised on how to perform quality control on data provided to DeepData, as the system does not currently have a way to control the quality of sequences submitted. One possibility is for DeepData to continually publish data so that these can be checked against other data sources such as the NCBI. Genome ID or taxonomy IDs would be useful as metadata to be submitted along with the sequence data. The SILVA database could also be used to check 16S quality, but this database is not as well curated as the NCBI. There is a general problem in assuring quality using well curated sequence collections that are trustworthy.

10. Participants also discussed the need for specimen sharing. Regarding microbes, scientists can access organisms from a culture collection. It is not clear how to access culture collections for other microbial groups. There was a suggestion for the ISA to establish a mechanism for contractors to develop and share collections during their baseline surveys. Suggestions were also made that the ISA could facilitate this effort as it is of interest to society to make the collections accessible or available in the public domain. Contractors could provide samples for cultivation or isolation of specimens and/or their derived products.

11. Consideration was given to the high-throughput sequencing technology and the depth of sequencing (for a wider coverage of taxonomic groups as well as higher-level genomic studies). In order to discover sufficient understanding, certain sequencing depth should be achieved. As for the sequencing errors, participants noted that combined sequencing technology can be used.

**Theme II: Q3. Which tools are required to improve species identification in different mineral provinces? Q4. What initiatives, networks, resources are available, desirable, and/or needed to support key taxonomic groups?**

12. Participants noted that so far there has been no established methodology for studying virome. It was noted that the study of virus in the deep sea is currently very difficult. A common method is to pre-treat samples for RNA or DNA and perform a nucleic acid extraction, and then amplify with random hexamer or nanomers. Participants also discussed if there are other tools beside 16SrRNA gene for studying bacteria or Archaea. Dialysis sampling technique was mentioned.

13. There was also a discussion on what tools are required to improve identification of microbial communities down to a species level using eDNA, particularly as it relates to knowing if the organisms were alive or primarily represented by relic DNA at the time of collection. Discriminating dead organisms or species that may not now occur in the CCZ can be investigated using the WoRMS database to check if organisms are common to the deep sea or use OBIS to quality control the sequence. It was suggested that eDNA data can be combined with other types of biological data (e.g., from OBIS records on species occurrence) to provide more robust results.

14. Participants also raised the issue of sampling the microbes associated with key megafauna groups (i.e., the microbiome), namely sponges. Sponges host an exceptionally rich and diverse associated microbiota, which is species specific and known to change with depth. This microbiota is a source of bioactive compounds, constituting a rich source of marine genetic resources, potentially

linking collections to bioprospecting interests, facilitating cost-sharing. The SponGES Horizon 2020 project has shown that 16S rRNA gene amplicon sequencing is capable of revealing this prokaryotic diversity. Also, most sponges are efficient filter feeders and recently it was shown that eDNA can be recovered from their tissue. Metabarcoding identified extensive fish, marine mammal and bird DNA reads from sponge tissue, suggesting that sponges are natural samplers of DNA. It was suggested that contractors can take opportunities to sample the sponge microbiome and consider options for using them as eDNA samplers.

### *Meiofauna*

15. Different regions, habitats (including midwater communities) and different taxa were considered. Most of the available technologies apply to all these areas. Participants were reminded of the main highlights of two previous workshops: the ISA workshop on Meiofauna held in Ghent in 2015, and Deep CCZ Biodiversity Synthesis workshop, held in Friday Harbor in 2019. Those highlights included: 1) meiofauna is very diverse but very few studies provide species/genus resolution data; 2) biodiversity assessment of meiofauna communities remains incomplete due to under-sampling; and 3) differences in methodologies and taxonomic inconsistency have prevented standardization of dataset. Therefore, standardization is required and new techniques may be useful.

16. The results of the break-out session discussion were compiled in six main topics as summarized below. A table, including an overview of available tools, their pros and cons, their readiness, and the actions required for standardization, was compiled in the appendix to this annex. A list of minimum requirements for taxonomical meiofaunal studies, covering sampling, storing, and processing of meiofaunal taxa, and biodiversity data analyses, is also presented in the appendix to this annex (paragraph 2) and further elaborated in the summaries below.

### **Building and maintaining a reference database of qualitative data, combining vouchering and barcoding**

17. Vouchers for species barcoding require very good images of specimens, but the quality of images is often very variable. In terms of standardization, it is important to identify which tools are the best. A single picture is not sufficient for most taxa. Ideally, a voucher requires a full description of the specimen to complement the barcode data, but this is not a realistic approach. It is also necessary to standardize temporary specimen identification, as suggested by Tammy Horton in her presentation (see summary in annex II). Minimal requirements for vouchering should be defined for specific meiofauna taxa to make data comparable; guidelines for specific taxa would be very useful. Confocal microscopy is one tool for visualizing morphology, but it is time consuming when specimens need to be processed quickly for molecular analysis. The equipment is also costly, and it does not allow observation of internal diagnostic features.

18. It is necessary to populate Genbank, but also to link it to a database with diagnostic characters. World Register of Deep-Sea Species (WoRDSS) offers the basis for doing this. Barcode Of Life Data System (BOLD) is also a tool to share data on morphology and DNA sequences. In both cases, the concern was raised about who is going to curate and edit the data and information.

### **Building and maintaining capacity in taxonomy in a long term**

19. There is a strong need to support new young taxonomists to ensure a critical meiofaunal taxonomic research and education for the next decades. It was suggested that training devoted to taxonomy could be supported by ISA contractors under the ISA contractor's training programme. As part of their social and scientific contributions, and obligation to invest in capacity development, contractors could be required to support taxonomy science with a significant component of local/national funding, to ensure cross-lab exchange between taxonomic experts and students from

developing countries. It was further suggested that contractors obtain feedback on the training achievements.

20. Long-term sustainability on taxonomic capacity (i.e., mainly well trained human capital) is needed to guarantee the availability of taxonomists in each taxon for meiofaunal identification during the exploration baseline studies and future monitoring, as well as to find potential methodological, technological and research gaps that may need to be addressed in future workshops/studies. High-performance meiofaunal networks are needed, including people to enable/support data acquisition, storage, management, integration, searching/compiling of data and references, analysis, visualization, and distribution of taxonomic data. Development of certification programs can be implemented for this purpose.

### **Ensuring quality of samples**

21. The first step in proper biodiversity research is an access to good samples. Box core samples are not suitable for meiofauna studies. This point has been already highlighted in the ISA workshop held in Gent in 2015. The revised LTC recommendations became available in 2019 with very distinct guidelines on meiofauna sampling in comparison to the previous version; this information should be clearly communicated to the contractors.

22. While some inconsistencies are observed in the recent version of the LTC recommendations in regard to slicing procedure, a degree of flexibility is needed because there are different acceptable practices. Therefore, it is important to identify a minimum standard and apply it with flexibility according to specific conditions, for instance, presence of nodules that prevent slicing).

### **How much data is needed for a proper environmental baseline?**

23. One of the key questions for the contractors is to know the minimum data requirements. It is likely impossible to identify all specimens to species level. However, time should not be a constraint. For example, monitoring work in the North Sea is conducted by other environmental consultancies, but in that region the fauna is well known; for the deep sea more time is needed.

24. Consideration was given to two possible parallel pathways: the first includes the detailed integrated taxonomic description of abundant (and rare) new species, and the second combines a high throughput approach (HTS, Maldi TOFF) with building a reference database.

### **Is there new technology that could potentially accelerate biodiversity research?**

25. A question was raised regarding the use of artificial intelligence (AI) in the future. Currently, there are sorting machines that can separate specimens into different vials, or identify specimens based on video analysis (continuous plankton recorder). These new tools are very expensive and work well in areas where species are known. It is already possible to identify deep-sea samples at a higher taxonomic level, while different organizations are further developing these tools, but they are not yet ready for species-level identification. Therefore, a mechanism is needed to bring taxonomists and engineers together for advancing these developments. In addition, there is a visualization lab that can make 3D scans and print the specimens; however, detailed morphometric plans and measurements are still required. Acquiring these systems would increase the costs for contractors and other subcontracted companies and would also limit the equitable access and use of these technologies.

26. At this stage, two parallel approaches are suggested: 1) technological development, exploration/discovery and high resolution, *versus* 2) specific, easily obtained data that address specific questions relevant for the impact assessments.

### **Are there other crucial actions to be considered for increasing the efficiency and quality of taxonomic research in a long term?**

27. Consideration was given to explore the extent of size-based modelling for allowing integration of data across broad size categories.

28. Biological collections are important source of specimens. Further consideration is needed regarding how samples should be stored for the long term, in which collections, and who will curate and take care of the long-term repositories, as well as the availability of all sizes and institutional types of collections for research and education, while ensuring long-term sustainability.

29. It is necessary to develop a culture of responsible stewardship for, and access to, biological specimens.

### **Macrofauna**

30. The results of the discussions are summarized below.

### **Theme I**

#### **Q1. How can quality assurance/control of taxonomic data be ensured? e.g. the role of voucher specimens, sample, and data curators, and intercalibration exercises.**

31. Participants considered the following steps *essential* to ensure quality assurance/control of taxonomic data:

- Specimen vouchering of **representatives of all species** in accessible collections in institutes for maintaining specimens in perpetuity;
- Publishing of the **associated data records** (the taxonomic information and associated information; e.g., site, collecting event) in an openly accessible database (e.g., OBIS and GBIF, or an institutional database that is subsequently harvested by OBIS/GBIF);
- Fully funded long-term system of curation and loans to enable **long-term access/sharing of specimens**, including data management/database maintenance; and
- Usage of **global data standards**, i.e., DarwinCore for recording all relevant taxonomic and associated data (site, collecting event, environmental/oceanographic info, location of samples), combined with proper usage of identifiers - global unique identifiers (GUIDs), for allowing linkages between databases and maximising traceability/discoverability.

32. Participants considered the following steps *desirable* to ensure quality assurance/control of taxonomic data:

- **Vouchers of all species records and archiving of unsorted specimens** in natural history collection facilities (not just representatives of species). Publishing of the related data records on openly accessible database as above;
- Use of **informal taxonomic names (Open Nomenclature)** linked to vouchered specimens, and natural history collection systems should be encouraged to make lower-resolution / informal taxonomic records available (e.g., unsorted specimen lots), for allowing their discoverability;
- Image repository of all specimens and **archiving of imagery and publishing on global databases** (e.g., institutional databases that are searchable, GBIF, Scratchpads). This could enable future AI-based identification;
- Publishing of **molecular data on Genbank** and BOLD; and
- Archiving **additional molecular vouchers, e.g., frozen tissue** and DNA vouchers, linked in records to 'parent' specimen vouchers.

**Q2. What are some actions/steps (short-term and long-term) needed to advance taxonomic knowledge in a standardized manner?**

33. Short-term actions considered by the participants include, *inter alia*:

- The ISA sets updated data standards (adequate metadata in addition to species checklist for all fauna from cruises) based on, for example, **DarwinCore**;
- Contractors and sub-contractors to **incorporate curation, access and databasing costs**;
- **Set annual targets for a number of specimens described/identified, curated, databased and made available with quality imagery** on global databases; e.g., for one PMN contract area in the CCZ 200 macrofaunal specimens/year, for one PMS contract area 50 specimens/year.
  - This way contractors, regulators, research community and others can **see incremental improvements year on year**; this would be key for motivating additional progress;
- **Distinguish clearly between physical specimens and associated data** in guidelines- these are two different (but interlinked) entities;
- **Annual stocktaking of curated/databased specimens/data available**; i.e., review of what data is available at what taxonomic level for all contractor data; and
- Effective involvement (e.g., regular meeting participation) of **existing/ongoing efforts in biodiversity informatics community** (e.g., GBIF/WoRMS/OBIS), need for robust directory/inventory at collections holdings level.

34. Long-term actions considered by the participants include, *inter alia*:

- Mentorship and capacity building /technology transfer for stakeholders with limited funds or experience of taxonomic works, curation, database workflows;
- Funded training programmes and career development for young systematists. Long-term structure to programmes/funding, allowing the development of skills required to become a specialist;
- Fellowships and regular posts in deep-sea taxonomy;
- Long-term funding streams to support taxonomic training above as well as storage and archiving of collections – funding/resourcing of natural history collection facilities;
- Communication to States, LTC members, ISA secretariat and other stakeholders on the importance of taxonomy and its potential contribution to fulfilling the ISA mandates.
- Regular forum/workshops with experts and relevant stakeholders
- Long-term mechanisms in place to share specimens and organize regular workshops for working-laboratory taxonomy to describe and identify taxa

**Theme II**

**Q1. Which tools are required to improve species identification in different mineral provinces currently under exploration?**

35. Participants considered the following tools *essential* to improve species identification in different mineral provinces currently under exploration:

- **Checklists** - comprehensive lists of taxa within region;

- ✓ Leading to the second step, i.e., **production of accredited keys and field guides**, which would be the ultimate aim;
- ✓ The above tools would ultimately lead to a position where **experts could provide QA/QC** with the majority of identification work born by contractors/consultancy community (some years away); and
- Continued **massive effort of DNA barcoding specimens** and providing access and imagery of vouchered, databased specimens linked to those barcodes.

36. Participants considered the following tools *desirable* to improve species identification in different mineral provinces currently under exploration:

- Massive development of **online image databases of identified specimens** to allow AI/cloud-based computational taxa identifications (e.g., iNaturalist);
- Engagement and **collaboration of taxonomists with the informatics/computer science community** to facilitate development of these tools;
- **DNA barcoding workflow for identification assistance**, e.g., a clearing-house barcoding system to allow those without molecular lab access to obtain barcode data for uncertain specimens; and
- Intercalibration workshops to encourage **joint taxonomic works**.

**Q2. What initiatives, networks, and resources are available, desirable, and/or needed to support key taxonomic groups?**

37. Participants suggested the following initiatives:

- More **focused online linkages** (e.g., Teams/Slack mini groups) and development of working groups - lessons learned from current covid-19 restrictions;
- Further **establish and develop collaborations** by leveraging existing networks and initiatives - DSBS, DOSI and others;
- In-person **workshops looking at specimens**, e.g., taxonomic workshops post-cruise; and
- Support for small collections, as well as large national level ones to **support a network of distributed collections**. This will help with distribution of risks among collections, also dissemination of capacity building opportunities, and increase accessibility.

*Megafauna*

38. The results of the discussions are summarized below.

**Theme I: Q1. How can quality assurance/control of taxonomic data be ensured? e.g., the role of voucher specimens, sample and data curators, and inter-calibration exercises/ Theme II: Q3. Which tools are required to improve species identification in different mineral provinces?**

39. Participants noted that megafauna is generally the only group where imagery-based sampling is considered in addition to traditional sample-based taxonomy. Imagery-based sampling inherently trades off a reduction in taxonomic resolution (i.e., may only be able to confidently identify an individual to family or order vs. genus or species) for an increase in spatial coverage.

40. For both sampling methods (images and physical samples), participants stressed the importance of establishing standardized protocols (“Gold Standards”) for sample collection and archiving to ensure the collection of optimal voucher material, along with robust associated metadata. Without the proper collection protocols, expensive collection efforts may result in unusable samples/images or limit their potential for taxonomic identification. Therefore, the initial effort and expense can be offset in the long-term – following the Gold Standards reduces the likelihood of having to repeat surveys.

41. Standardized protocols are the only way to ensure comparability between datasets collected in different areas, which is key for management purposes and for contractor’s requirement to assess regional distribution of species and communities/assemblages as well as genetic connectivity of key and representative species. These standardized protocols should be designated as the minimum requirement for conducting subsequent EIAs, and should involve all aspects from survey design, data acquisition, processing, and storage, leading to the generation of robust biological data.

42. Further importance was placed on obtaining useable imagery of collected specimens (in situ and after collection). A high-quality image showing different orientations of the specimen, could reduce the need for samples/taxonomists to travel to examine specimens, and provide increased taxonomic resolution to imagery-based surveying. Copies of images should be housed at natural history collection repositories with the archived specimens as part of their online databases.

43. A series of workshops may be needed for experts to create these specific protocols (see below).

44. There was general agreement that standards for ROV-collected taxonomic specimens include:

- Good quality *in situ* image(s) of the specimen prior to collection (see seabed imagery below); in the case of large specimens that are only partially-collected, this includes good images of the whole specimen with a scale, and set of macro close-ups;
- Metadata associated with the specimen collected;
- Protocols for appropriate DNA sample extraction and storage;
- Protocols for fixation and preservation of voucher specimens;
- Protocols for ex-situ photography associated with each collected specimen (e.g., at-sea photographs with scale prior to preservation); and
- Key and representative specimens should be the first priority, followed by other taxa, to fulfil the requirements for the baseline assessments.

45. Suggested standards for seabed imagery (subject to further review and discussion) can include, among others:

- Image stills should be priority over video (e.g., easier scaling and storage);
- Minimum image resolution to be set to maximize and standardize the detectability of megafaunal specimens;
- Maximum altitude of image collection above seabed should be set (e.g., 2-4 metres); and
- Minimum lighting requirements.

46. Participants stressed the need for specimens to be deposited in long-lasting and accessible repositories (e.g., regionally-oriented natural history collection facilities such as museums and other voucher collections) with appropriate curation protocols, storage facilities, and stable funding to ensure long term availability of samples, with the associated cost being considered in the survey planning stage. Contractors may be interested in subsidizing such repositories to ensure the long-term maintenance of such collections.

47. Participants discussed the use of a common nomenclature in biological data reporting to assist in data intercalibration. For instance, using OPEN Nomenclature to acknowledge uncertainty in specimen identification (see Tammy Horton’s presentation summary in annex II to this report; terms include *Stetit*, *Indeterminabilis*, and *Incerta*).

48. Quality assessment/control of taxonomic data and appropriate intercalibration exercises were discussed multiple times during the session, with the following points to summarize:
- In image-based assessments, work is required for a better understanding of the differences between conducting surveys with different platforms (e.g., ROV, AUV, and/or towed cameras), as very little research has been done in this regard. Intercalibration between different platforms is essential to ensure the comparability between data collected in different areas;
  - Setting up different taxonomic working groups within the ISA could be considered to review data submissions prior to depositing in the DeepData database. Such a taxonomic working group would act as a pool of experts to support quality assurance of datasets. Different pools of experts could be listed, e.g., for different regions, habitats, or taxonomic groups;
  - Consider setting up a certification for identifiers (with criteria to be developed) with a possible requirement for data submissions to be validated by one or more certified taxonomists;
  - Regular intercalibration exercises between contractors and experts to ensure compatibility and minimize observer bias in morphological evaluation of specimens; and
  - Reanalysis of a percentage of data by an independent lab to ensure quality control. These costs to be factored into the cost of the overall analysis.

**Theme I: Q2. What are some actions / steps (short-term (ST) and long-term (LT)) needed to advance taxonomic knowledge in a standardized manner? / Theme II: Q4. What initiatives, networks, resources are available, desirable, and/or needed to support key taxonomic groups?**

49. Capacity development was identified as a **long-term action**. When discussing training needs, a distinction was made to clarify the term “taxonomist” (an expert in a particular taxon who can identify and describe new species) from “identifiers” or “parataxonomists”, who are needed to identify and sort samples from a collection event. This categorization is based on publication track record rather than individual declaration. This is a 2-stage procedure for processing and identifying biological samples, with distinct training needs for each stage/role. A parallel 2-stage process is also used in image-based analysis, as discussed in the points above related to image analysis QA/QC. There is a need for both types of expertise to complete this process.

50. An emphasis was placed on developing a network for exchange of taxonomic expertise and knowledge/data. Discussion focused on:
- Enhancing/facilitating contactor support in the training and engaging of taxonomic experts. The need for taxonomic expertise will increase as minimum standards are set by the ISA on the collection and generation of robust biological data. This should be seen as an opportunity to promote the training of experts, e.g. in academia (PhD programmes) or industry (e.g. environmental consultants), which can be supported by contractors and facilitated by the ISA;
  - Creation of a metadatabase within the DeepData portal (managed by the ISA) was identified as **short-term action** needed to hold key information related to the collection of biological data. This metadata database would also serve to detail experts and institutions with experience in particular mineral provinces or taxonomic groups. This metadatabase can build on existing initiatives. Data needed for each separate submission to the metadatabase should include:
    - Specimen(s) collected;
    - Expert and institution that collected the specimen;
    - Expert and institution where the specimen is stored;
    - Locational data of the sampling location;
    - Whether in situ and/or ex situ images are available;

- Whether material for genetic analyses were collected; and
- GeneBank/barcode sequences, etc.
- Novel concept for a taxonomic exchange service can be, potentially supported by using small grants to cover travel expenses. The purpose would be to allow taxonomists to visit other laboratories, research institutions and/or consultancies working with biological data for 1-2 week periods. This work could be in collaboration with data curators and/or lead to the organisation of taxonomic workshops where they are most needed. It is ultimately more cost-effective to send 1-3 experts to one place compared to having 80+ people travelling to meet the experts, particularly for developing nations. This also reduces the need to ship specimens outside of the region of collection.
- Regional workshops can be organized also on-site or online (webinars) to train “identifiers” or “parataxonomists”. These identifiers could then form ongoing networks with their trainers. It is important to bring experienced taxonomists together with early career scientists. Recording these workshops (and uploading to DeepData) would generate online resources with many possible formats possible to further support methodological standardization, such as:
  - Guides on sampling strategies and protocols;
  - Tutorials for biological sample or image processing; and
  - Identification guides for particular taxonomic groups, etc.
- Topics and content of these potential series of workshops could be designed to enhance contractor engagement (e.g., selecting areas where contractors lack/need expertise). Tentative workshop series could cover different themes/categories, including:
  - Regions (e.g. East Pacific, West Pacific, Indian Ocean, North Atlantic, etc.);
  - Habitats (e.g. nodule fields/abyssal plains, ferromanganese crusts/seamounts, hydrothermal vents);
  - Animal groups (e.g. by Phylum-Cnidaria, Echinodermata, etc., by functional group - suspension feeding, deposit feeding, etc.).
- Enhance capacity building through specific training opportunities, such as: the MABIK initiative to train female taxonomists; creation of ISA/contractor scholarships for participation in taxonomic workshops, expeditions, conferences, accessing museum collections, etc. The ISA website could be used as a platform to advertise such opportunities.

51. Further QA/QC issues particular to image-based megafaunal assessments were discussed, as summarized below:

- Megafauna morphotype catalogues for different regions/habitats should be created and made available online to support future standardization of image-based megafauna analyses;
- The ISA DeepData platform was considered to host megafaunal catalogues as it is designed to be a long-lasting online platform, and should be accessible/familiar to contractors and researchers in the field. This would facilitate the addition of new taxa as contractor/academic work progresses in areas not previously surveyed;
- Links or uploading of catalogue data to other repositories (SMarTaR-ID, OBIS, WoRMS) should be explored to take advantage of extra functionalities offered by these platforms;
- The implementation of protocols for collaborative image annotation should be promoted. For instance, 2-step image analyses facilitated by online annotating software, such as Biigle. Using specially designed tools, non-experts can conduct specimen detection (1st step), and trained experts can then perform subsequent identification to morphotype level (2nd step). This approach allows remote interaction among experts and between experts

and non-experts (e.g., facilitating discussion, taxonomic supervision, or training), and is hence well suited to promote capacity building, particularly if coupled with workshops or seminars to improve/share taxonomic knowledge;

- After morphotype catalogues have been made available online, the addition of new morphotypes and frequent necessary changes to the existing catalogue as knowledge progresses could be supervised by members of taxonomic working groups (e.g., Image-based megafauna expert group);
- Development of an archive for annotated image and video data would enable open audit, support future training of image annotators and enable/enhance the implementation of AI approaches. AI methodologies and algorithms have shown great progress in recent years, and efforts should be put in place to continue developing AI routines for complementing and speeding up image annotation protocols.

Appendix to Annex III

1. The table below provides an overview of existing tools at different stages of readiness. Advantages and disadvantages in a taxonomic context are listed, especially for remote, highly diverse but under-sampled areas.

<i>Tools</i>	<i>Pros</i>	<i>Contras</i>	<i>Action required</i>	<i>Readiness</i>	<i>Scientific Questions addressed</i>
Light-Microscope photos up to highest possible magnification	Can be archived and easily shared with other taxonomists.	Requires clear knowledge of structures to be depicted and obtain multiple shots at different levels to depict microstructures.  Photos must be of very good quality and show the relevant structures for identification and this is not always the case.  Cannot distinguish cryptic species; requires several specimens in case of gender and developmental stage differences.  New HDD photographic strategies require larger storage capacity.	Set minimal requirements (compared with passport picture) for specific taxa; requires minimum infrastructure (i.e., phototube, camera, cables, microscope with details on objectives and eyepieces, illumination systems, contrast, software, PVC, memory, maintenance cost).  Capacity development is required for mounting techniques, slide preparation, mounting (detailed guidelines required) staining techniques, and photography recording and processing.	High	Macro-ecological and biodiversity questions
Light microscope video	Can mimic what is observed down the microscope. Allows imaging through the specimen specimens can be on a temporary mount, and then be used for molecular analysis. Audio could be added to explain details or highlight critical aspects shown in video.	Time consuming; good quality interference contrast microscope and video needed; video editing software; requires clear knowledge of structures to be depicted and obtain multiple shots at different levels to depict microstructure; requires several specimens in case of gender and developmental stage differences.  New HDD photographic strategies require larger storage memory.	Video files can be shared and the specimens examined and still images taken from the video. Requires minimum infrastructure (i.e., phototube, camera, cables, microscope with details on objectives and eyepieces, illumination systems, contrast, software, PVC, memory, maintenance cost).  Capacity development is required for mounting techniques, slide preparation (detailed guidelines required) staining techniques, and photography recording and	High	Taxonomy, biodiversity, and community ecology

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<i>Tools</i>	<i>Pros</i>	<i>Contras</i>	<i>Action required</i>	<i>Readiness</i>	<i>Scientific Questions addressed</i>
			processing. Perhaps also to provide a template for how the specimen should be orientated for photography; templates will also be useful for descriptions.		
Drawings/Illustration	Reveal three-dimensional result that is not easily achievable with photos.	Need to be well done and add value to the picture. Time consuming. Can be computer-aided: cf. Coleman, C.O., 2003. "Digital inking": How to make perfect line drawings on computers. <i>Organisms Diversity &amp; Evolution</i> 3, Electr. Suppl. 14: 1-14.	A light camera ( <i>camara clara</i> ) or projector, or drawing tube is needed in addition of the microscope.	High	Taxonomic, macro-ecological and biodiversity
Identification keys - dichotomous	Give the needed characteristics to identify a specimen.	Not helpful if clear terms to describe structures are not used, or if key characters are missing.	Integrate open access repository of published keys; engage in regional capacity building efforts.	Taxa specific	Identification
Identification keys - pictorial	Easy and user-friendly	Not helpful if drawings do not show clear differences.	Initiate effort that involves art students to support with HDD microphotographs and drawings to illustrate ID keys; capacity building needed.	Taxa specific	Identification; biodiversity
Literature	Indispensable tool, using the latest publications and keeping up with the changes.	Needs to be updated and include also the less accessible journals.	<p>Create open access repository articles, book chapters, books, reports, reviews. Promote that older keys and drawings are available in the Biodiversity Heritage Library</p> <p>Useful or important articles still not available from major digital libraries (e.g., biodiversitylibrary.org) could be deposited for download at ISA-maintained website.</p> <p>For Nematode taxonomic and ecological literature, Nemys an online tool is available and further work</p>	Taxa specific	Identification; biodiversity

**ADVANCED COPY FOR WEB-POSTING**

<i>Tools</i>	<i>Pros</i>	<i>Contras</i>	<i>Action required</i>	<i>Readiness</i>	<i>Scientific Questions addressed</i>
			is in progress, with articles on new species being continuously added. All subscribed users have full access to PDFs. <a href="https://nemys.ugent.be/">https://nemys.ugent.be/</a>		
Scanning Electron Microscopy (SEM)	Shows structures not seen with optical microscope.	Time consuming and not enough material available; SEM microscopes not accessible on a routine basis	Larger amounts of funds are required to count for this equipment cost, although it has diminished, Recent models have new capabilities, size has been reduced, use is technically simpler making them more attractive and affordable almost like a larger more complete light microscope. Specimens or biological material are consumed during research investigation unavailable for later molecular or biogeochemical studies.  Training and capacity building are required. Cost and availability of parts, their import process and maintenance may be limiting to some institutions.  Hiring a specialist to operate and maintain the equipment is difficult for many institutions.	High	Identification; biodiversity
Confocal microscope	Using the auto fluorescence properties of the nematodes, some structures can be easily highlighted; retains morphological details of taxa deformed by formalin fixation.	Very expensive equipment and requires lot of time to reach good results. It will always depend on the auto florescence of the species..	Useful for better understanding the diversity of species hosting symbionts and relying on specific biogeochemical processes, i.e., chemosynthesis.  Training and capacity building are required. Cost and availability of parts, their import and maintenance may be limiting to some institutions. Hiring a specialist to operate and	High for some taxa	Taxonomy

<i>Tools</i>	<i>Pros</i>	<i>Contras</i>	<i>Action required</i>	<i>Readiness</i>	<i>Scientific Questions addressed</i>
			maintain the equipment could be prohibiting for many institutions		
Bar coding	In principle provides certainty on the species identification	<p>Some incorrect morphological identification has led to mistaken barcoding identification.</p> <p>Vouchering can be time consuming Not that successful for smaller nematodes, which dominate the deep sea (e.g., <i>Monhystrella</i>).</p> <p>COI gene does not work well for nematodes.</p>	<p>Integrate new molecular-only collections.</p> <p>Capacity building required in processing the sample and analyzing the data, software use required. Genome projects may provide phylogenomic framework to identify. Increasing number of sequences will require cloud and digital infrastructure. Comparison and confirmation of identification of non-preserved sequences. New taxa described.</p> <p>“Orphan” records will require careful curation knowledge. Literacy needed in many regions/nations.</p>	High	Identification, taxonomy
Meta barcoding	<p>Time saving.</p> <p>Less expensive in the long run than morphological ID.</p> <p>High performance in combination with good reference database.</p>	<p>It does not identify specimens individually.</p> <p>No information on gender.</p> <p>You can miss information on ecology.</p> <p>Lack of proper reference database.</p>	Same comments as above.	High	Community analysis, phylogeny, biodiversity estimates, connectivity

<i>Tools</i>	<i>Pros</i>	<i>Contras</i>	<i>Action required</i>	<i>Readiness</i>	<i>Scientific Questions addressed</i>
High-throughput imaging and AI/algorithm training (e.g., zooscan/zooimage, flowcam, holographic microscope)	Fast recognition, large-volume processing	Confidence for higher-taxon classification but generally low resolution. Needs further investment, initial expense high. but rewards can be significant.	Identify (standardize) methods for specific ecological questions. (needs further development and integration with workflow pipelines (retrieval of specimens that have been imaged)). Currently used for plankton samples but limited demonstrated use for infauna ISIIS plankton imager ROTVs and Optical systems ( <a href="https://www.planktonimaging.com/">https://www.planktonimaging.com/</a> ) Funding to acquire the equipment, training and capacity building needed to deploy, maintain the equipment, process images, catalogue. Cloud, AI and machine learning required.	Moderate to low	Impact assessment on higher taxon level, higher-taxa ecological questions (more indicator research needed to support efficiency)

2. Minimum requirements to be identified for meiofaunal studies related to biodiversity research includes:

- ✓ Minimum requirements for assessing abundance of higher taxa (how many specimens);
- ✓ Minimum requirements for in situ sampling and storage/accessibility;
- ✓ Minimum requirements for sorting into higher taxa;
- ✓ Minimum requirements for quantitative species identification (how many individuals per species) (monitoring);
- ✓ Minimum requirement for species description (baseline data, which species; drawing, SEM, Confocal, barcoding);
- ✓ Minimum requirements for qualitative species identification (how many species); and
- ✓ Minimum requirements for connectivity analyses of abundant or key-species.

*Annex IV*

**Summary of Panel Presentations**

**Tim O'Hara (Natural History Museum Victoria, Australia)**

Mr. O'Hara has collaborated with scientists in Britain, USA, Germany and China to identify and describe ophiuroids from the CCZ region using both morphological and DNA sequence data. There are at least 45 species now known from the area. His experience looking at these animals indicates that: 1) in-situ photographs can rarely be identified to species; 2) there are currently no consolidated tools to identify CCZ animals, therefore a taxonomic expert is required to assist in the identification; 3) there are several cryptic species complexes known from DNA sequences that cannot be distinguished morphologically; 4) there are a number of 'dark' species that are well characterised by DNA but are known only from damaged or juvenile specimens; and 5) the combination of DNA barcodes COI and 28S are required to both distinguish species and allocate them to the correct taxonomic position (family & genus). The barcode 18S is too conserved to be useful, as it is very similar for most ophiuroids.

Future emphasis could be given to the following four actions. Firstly, generating barcodes for all taxa. The gold standard for animals would be to sequence the entire mitochondria (including COI, 16S/12S) and the nuclear ribosome (28S/18S) complex. This would allow further flexibility for future development of eDNA protocols. Secondly, preserving voucher specimens in natural history museums. Thirdly, funding projects to describe the animals and producing morphological keys. This is feasible for 45 currently known species. Lastly, enhancing the Open Nomenclature system to add "cryptic-complex" and "form-habit" levels. The first would allow the naming of a group of animals that are so close that they cannot be separated morphologically. The second would be an official name that could be used for image annotation (e.g., basket star is a form of ophiuroid that has branching arms but cannot be assigned to a single taxon).

Further consideration could also be given to the scale of biodiversity changes over contract areas. Since we now know nodules are a key habitat for many species, their complete removal could result in global extinction of some taxa. Since the APEIs are situated outside the main nodule area, nodule extraction could be spatially managed within each contract area as a mosaic, leaving some areas of nodules untouched. Moreover, the timing of extraction could be rotated around the contract area, facilitating the recovery of the fauna from nearby untouched areas. Key management questions are therefore: 1) at what spatial scale does biodiversity change across the nodule field; 2) what is the scale of the impact footprint (including resettling sediment); and 3) how long does the soft sediment fauna take to recover. The mosaic could be designed to encourage contractors to move to extraction methods with less environmental impacts.

**Chong Chen (Japan Agency for Marine-Earth Science and Technology-JAMSTEC, Japan)**

Taxonomists need actual specimens to carry out their work. Currently the ISA requires contractors to submit environmental and geological data, but there is a lack of oversight on physical specimens. National museums and public collections exist not only to safeguard specimens but also to actively facilitate global loans that allow specimens to be used by the relevant scientists. Specimens collected by ISA contractors, however, are often not accessioned at such collections, rendering them accessible only to scientists connected to the contractors. As such, many specimens collected from the physical abyss quickly sink to a metaphorical abyss, being invisible and unavailable to taxonomists. Ensuring the sharing of specimens through depository at permanent, accessible homes for collected specimens at recognized public collections to make sure they are used, and that they can be used, should be a key feature of any taxonomic collaboration platform. For example, contractors may have priority loans for a certain period from the museum initially, after which the specimens are retrieved by the museum and become open to all taxonomists. Another important reason for accessioning specimens in major museums is that they open all data to major biodiversity databases such as Global Biodiversity Information Facility (GBIF), making

distribution data immediately available to global scientists. Care should be taken, however, to avoid accessioning at ‘dark’ collections that do not actively facilitate open loans to global scientists. Small collections can also be useful if they make global loans.

The taxonomic collaboration platform should not only facilitate taxonomy itself, but also ensure that taxonomy feeds into key conservation tools. As an example, the IUCN (International Union for the Conservation of Nature) Red List of Threatened Species has been credited with significant conservation benefits. Last year (2019), the Scaly-foot Snail or Sea Pangolin (*Chrysomallon squamiferum* Chen et al., 2015) became the first deep-sea species to be assessed and listed as Endangered from extinction risks from future deep-sea exploitation activities. As of now (September 2020), a total of 61 assessments for hydrothermal vent endemic species across the globe (31 published and 30 upcoming) have been completed using a rapid assessment matrix. Of these, 10 species were assessed as Critically Endangered, 21 Endangered, 12 Vulnerable, and 6 Nearly Threatened. All 12 assessed as Least Concern occur within Marine Protected Areas or areas governed by the Antarctic Treaty. The same assessment method can be applied to insular habitats such as seamounts (i.e., ferromanganese crusts). The ISA could consider integrating such conservation tools in the training (e.g., how to assess species for the IUCN Red List) as part of the taxonomic collaboration platform.

**Samantha Smith (Global Sea Mineral Resources-GSR, Belgium)**

There are two important themes in this discussion: exploring mechanisms for collaboration and capacity building. As it has been discussed, there are two areas of collaboration: between taxonomists and between contractors and taxonomists. Contractors are not taxonomists, and they need guidance and advice from taxonomists. Contractors also need standardized methodologies to ensure consistency in the results from different areas. It can be useful to have small working groups on different taxa. These groups can get together to inform the ISA about standard methods, so that studies can be compared at a large scale. Contractors in the eastern Clarion-Clipperton Zone rely on the same taxonomists to collect taxonomic data. As such, it is relatively easier to carry out a comparative analysis. Other contractors may also explore similar mechanisms. Having a centralized database to host all data is important. DeepData is set up to achieve this end and to make the data accessible. Contractors also need clear, consistent and stable instructions about the data required by the ISA, while bearing in mind the purpose for data collection is to support environmental impact assessments (EIAs). It is necessary to know what questions need to be answered, and the needs of scientists and the ISA may be different. For example, when contractors propose a preservation reference zone, they need to know that this zone is not going to be impacted by mining. The scale and resolution of data collection may also be different between contractors and scientists. Creating an APP for experts to comment on taxonomic identification can also be helpful. With regards to capacity building, contractors’ resource can be best used to address the “bottle neck” in taxonomic training. Contractors rely on taxonomists to identify what is most needed, such as sponsoring a PhD student or lab training.

**Koh-Siang Tan (Ocean Mineral Singapore-OMS, Singapore)**

A fundamental pre-requisite to exchange taxonomic expertise and techniques is the availability of well-preserved specimens associated with robust metadata, including images obtained prior to preservation, if possible. Historical material notwithstanding, current methods of collection and preservation onboard vessels therefore need to be standardized as far as possible, with the aim of ensuring long-term morphological and molecular integrity of biological material. Methods of preservation may differ for different taxonomic groups, and this may need to be taken into account. Meaningful discussions on taxonomy can only take place if specimens are properly preserved in the first place and available for studies.

Apart from the specimens, digitalized data associated with each specimen are increasingly the first point

of reference for any international collaborative effort. The inclusion of good quality digitalized images that are useful taxonomically would provide considerable advantages in the early stages of identification, particularly for ‘dark taxa’. A set of ‘best practice’ reporting guidelines for images (which will differ across different taxonomic groups) could facilitate knowledge exchange when the actual specimens are not available. Such guidelines could conceivably include, e.g., what parts of the specimens should be imaged, how the part of the specimen should be orientated in the image, and what imaging technique to adopt etc. The issues surrounding the continued availability of a sufficient number of competent deep-sea taxonomists across the exploration and exploitation timelines in the CCZ are real, urgent and complex. Training taxonomists ultimately requires mentorship and institutional support to facilitate participation in cruises, as well as access to specimens, collaborators and necessary facilities to study deep-sea material. Regular taxon-specific training and discussion workshops with achievable objectives are useful for mentors, practitioners and would-be taxonomists alike and should be continued. However, a critical longer-term goal is the sustainability of taxonomic and ecological expertise for a wide range of organisms through the exploration and exploitation phases. A simple solution is not in sight, but a plan needs to be in place sooner rather than later. Regulatory requirements towards this end may be a consideration.

**Tina Molodtsova (P. P. Shirshov Institute of Marine Biology of Russian Academy of Sciences, Russia)**

First, it should be acknowledged that deep-sea taxonomy is critically needed. Despite many methods evolved in the last decades, routine and robust taxonomy is still needed to identify species, describe new species, and calibrate all fast-evolving methods. Taxonomy does not exist without taxonomists, and it is a skill and one has to be trained - or self-trained for years to become a taxonomist. This skill cannot be acquired easily with minimum training - it has to build on a personal experience and sustained involvement in taxonomic studies and training. It has to be acknowledged that existing deep-sea taxonomists have unique knowledge and expertise, and it is necessary to benefit from this existing expertise and knowledge. The existing deep-sea taxonomists have to be the source of knowledge and the base of the platform for taxonomic expertise. For proper expertise, intercalibration is needed, and it has to be done at the stage of exploration studies, before the exploitation. Intercalibration needs to happen between taxonomists working in the same area, different working groups, and between different methods (like ROV vs. AUV or baited traps studies). This kind of taxonomic intercalibration needs to be a continuous process and a collaborative effort, and the ISA can encourage and support such collaboration.

It is also crucial to train and encourage new taxonomists, and to encourage experienced taxonomists to share their knowledge. There are many ways to bring basic knowledge that can evolve further. Basic taxonomic knowledge may be transmitted in a series of webinars or a series of regional training workshops (may be in connection with scientific conferences – like DSBS in 2021 or other ISA events). The same meetings can be used as an intercalibration platform. Contractors can provide opportunities for at-sea training programs, as well as museum curation, taxonomic exchange programs, and virtual workshops.

**Magdalena Błażewicz (University of Lodz, Poland)**

Taxonomy constitutes a basis for biological and ecological analyses. It needs to be emphasized that no biological analysis can be truly meaningful and complete without a thorough taxonomic approach. Therefore, the importance of taxonomy needs to be reiterated and understanding of taxonomy by a modern society should be enhanced. Taxonomy is crosscutting field for ecology, functional biology and phylogeography. Moreover, it is fundamental for any biological analysis and conservation planning. Long-term actions for promoting taxonomy as a cross-cutting field and fundamental to other fields of scientific inquiry are necessary; in addition, such actions need to involve working with the public and social media. Significant achievements of the Census of Marine Life include several useful platforms (e.g., OBIS, WoRMS, INDEEP, ResearchGate). Although all of them are very useful tools, they are managed by scientists and target scientists as their main audience. With this in mind, efforts for giving taxonomy a modern face should be directed to those who remain unconvinced of its importance. The society’s role in, and responsibility for, protection of the marine environment is well recognized. The deep sea is so remote, distant and isolated, leaving many with a feeling of uncertainty and a lack of awareness.

Twenty years ago, the scientific community was alarmed by the fact that many taxonomists were approaching retirement and their knowledge may be lost. It was evident that a new generation of taxonomists should be trained. Twenty years later, the situation has not improved. We feel there are fewer taxonomists now compared with twenty years ago. The training of a new generation of taxonomists requires not only time and financial support, but also a better perspective for young taxonomists in securing long-term jobs and grant support. The training of young taxonomists can include opportunities for new post-doc positions offered by various museums and academic centres. In addition to training full-fledged taxonomy experts, taxonomy expertise can be transmitted via a series of short-term visits aimed at offering a large variety of training opportunities in various segments of integrative taxonomy (morphology, imaging, cataloguing, morphometry, genetics, ecology). Such visits could be integrated into the ISA-supported training schemes, so that those schemes are better focused and address the needs of environmental monitoring and impact assessment. The time spent on training a young scientist under the supervision of an experienced taxonomic expert can be crucial for long-term capacity building.

**Sarah Samadi (Museum of Natural History, France)**

The Tropical Deep Sea Benthos (TDSB) program has collected samples from 7,500 stations since 1976, at depth ranging from 100-1,500 meters, and led to about 2,000 scientific papers and more than 4,000 species described. Key features of the TDSB program include the involvement of a large network of taxonomists, a clear publication policy, and registering the specimens and the metadata in public repositories/databases (mainly at MNHN- Muséum national d'Histoire naturelle).

Results show that: 1) 40% of the identified species were sampled only at one location; 2) the number of specimens are small and density is low; and 3) physical sampling and accurate taxonomic identification are needed to analyze the structure of communities and connectivity at various scales. A recent cruise in 2019 surveyed 3 seamounts near New Caledonia, and through working with a large team of taxonomists on board, many specimens were collected and identified. The experience showed that it was very difficult to identify species from images, and physical sampling at the same locations is needed to provide accurate identification results. Experience from the TDSB program has demonstrated the importance of collaborative work at sea to accurately sample all the components of fauna. Taxonomic workshops after completing the cruises can also be helpful, to enable efficient identification and databasing, exchanges between expert and junior taxonomists, and to define how to identify specimens from images in an accurate way. Finally, encouraging publication and dissemination of the results are also important for sharing knowledge and raising awareness.

**Mauricio Shimabukuru (ISA Secretary-General Awardee, Brazil)**

Despite the increase of species description in the deep sea over the last years, many species remain to be described. In many biodiversity assessment studies, the 'species list' is in fact a list of morphospecies which makes it hard to compare among different studies in the Area. The inclusion of DNA data makes the morphospecies list comparable between different studies since the sequence data are available by existing online platforms. However, researchers often face the choice between preserving samples for molecular or morphological identification. Even having a specimen available for both methods, the number of individuals per 'species' and/or incomplete/damaged specimens make impossible a formal description of a new species according to the International Code of Zoological Nomenclature. To make different studies comparable, sharing not only the DNA data but also images from the organisms should be encouraged, as well as brief morphological notes to distinguish the species. This will ensure that different studies using different methods can use the same platform. BOLD System is an example, since each record allows the inclusion of images and brief and/or detailed notes of the specimen as well as the DNA sequence. The expertise to taxonomically classify an organism is not something that you can quickly learn. For this reason, taxonomic training (in different group of animals) is a key factor to effectively enhance deep-sea

taxonomy in a way that ensures quality in species identification. Taxonomic training programs will also facilitate the sharing and exchanging of the knowledge among relevant experts and encourage collaborative efforts, with a particular emphasis being placed on those from developing States.

**Jinwook Back (National Marine Biodiversity Institute of Korea-MABIK, Republic of Korea)**

First, the key feature of the platform facilitating the exchange of deep-sea taxonomy expertise and techniques should be encouraging taxonomists to be engaged with various stakeholders. Since the establishment of MABIK in 2015, more than 20 full-time, tenure track taxonomists have been conducting individual and joint research. Encouraged to pursue inter-disciplinary and joint research efforts, MABIK taxonomists carry out research on the taxon they specialize in as well as other taxa. This inter-disciplinary joint research expands to exploration of marine genetic resources, commercializing of new natural products, designing outreach programs and supporting international policy making. This inter-disciplinary collaboration has been successful particularly in securing research funds, which supported implementing new research projects and hiring new taxonomists. At the core of this inter-disciplinary and cross-sectoral collaboration lie 16 designated institutions and MABIK's Data Base System MBRIS. As a hub of 16 designated institutions, MABIK collects samples according to its standardized methodologies, the samples are classified at a Phylum level. If MABIK cannot undertake necessary taxonomic analysis, the sample is transferred to one of 16 designated institutions. After analysis, the result and information come back to MABIK's Data Base MBRIS. Specimens will be returned to MABIK or stored separately in each storage facility. Second, the suggested training methodologies and activities to enhance individual and institutional capacity related to deep-sea taxonomy is to provide taxonomists with: 1) inter-disciplinary and cross-sectoral work experience; and 2) opportunities for actual practice. Opportunities for experiencing inter-disciplinary and cross-sectoral work such as collaboration with legislators, policy makers and journalists would result in securing a sustainable financial and human resources and raising public awareness of taxonomists and taxonomy. Although enhancing taxonomists' capacity to collaborate with other stakeholders is essential, capacity building in taxonomy should not be underestimated. The actual practice of identification and classification becomes the greatest asset in dealing with a sample with no taxonomic keys and dark taxon. However, in deep-sea taxonomy, there are few chances to practice species identification. As such, building a practical and mutually beneficial mechanism to share the samples among different institutions would allow more opportunities for taxonomists to be trained through actual practice. Since the number of samples from deep sea would be limited, utilizing digital specimen for training and online education programs or workshops could be an option to consider.

**Ward Appeltans (Ocean Biodiversity Information System-OBIS)**

The Ocean Biodiversity Information System (OBIS) is a project of the International Oceanographic Data and Information Exchange (IODE) programme of IOC-UNESCO and is recognized as a global open-access data and information clearing-house on ocean biodiversity. OBIS currently integrates 65 million occurrence records of 137,000 marine species from over 3,000 different databases. However, compared to the shallow and coastal areas, the deep-sea (below 500m) remains underrepresented with close to 2 million records of 26,000 species. Within the framework of a Memorandum of Understanding between the ISA and IOC-UNESCO, we are currently working out modalities to link data of ISA's DeepData with OBIS. Expanding the global data commons will provide a much more valuable source of information to aid taxonomy, e.g., in discovering new records of species in areas of interest (including newly described species and possibly in the future temporary names of yet undescribed species). Combining trait information from the World Register of Marine Species and data attributed to records in OBIS such as depth information also provides powerful tools for quality control, such as to filter out DNA sequence data from marine snow (dead shallow-water organisms). With the growth of DNA-based occurrence data, OBIS will develop a number of tools to improve data quality, such as a taxonomy "blast" tool for regular reprocessing DNA sequences in OBIS in order to update the species identifications against updated references databases. In addition, a sequence lookup service will be built which will allow uploading newly acquired sequences and comparing them with known sequences of organisms in DNA banks (including

OBIS) and provide back a list of records as well as a map showing the locations where these sequences have been found before. In other words, these global taxonomic and biogeographic databases are important tools for cross-referencing and validation of new data.

Regarding capacity development, ISA's draft Action Plan in support of the UN Decade of Ocean Science for Sustainable Development proposes a partnership with IOC-UNESCO and OBIS on training. IOC's Ocean Teacher Global Academy (OTGA) will facilitate training within the framework of the Ocean Decade and is designating specialized and regional training centres (currently 16 candidate centres). OTGA has been developing a portfolio of packaged courses which can be delivered face-to-face and/or online (blended learning). The IOC training course and certification of the identification of Harmful Marine Microalgae is an annual course geared for professionals in charge of public health and water quality assessment. This certification course (which includes lab-intercalibration exercises) could be a model to train the next generation of taxonomists and para-taxonomists (i.e., the species identifiers as part of biodiversity monitoring programmes).

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